



YAM20052.TXT

SEQUENCE LISTING

<110> National Institute of Agrobiological Resources, Ministry of Agriculture,
Forestry and Fisheries
Japan Science and Technology Corporation

<120> A NOVEL GENE FOR CONTROLLING LEAF SHAPES

<130>

<140> JP

<141> 2000-03-23

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 2468

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (198)..(2270)

<300>

<400> 1

```
aaaaaaatat ttcaaatcac actacactct ccgtcgtctc ctctcctctc ctctcctccc 60
cctctcctcc gcctctctcg catctgaggc tccgatcgcc ggcgacccca gccagaatcc 120
gccgccccgt ctcgccctcc ccgctcgacg agaccgcgcc gagcggcgaa gaggcctagt 180
gttcttcgca cctcgcg atg agt agc gcg gtg aag gac cag ctt cac cag      230
                Met Ser Ser Ala Val Lys Asp Gln Leu His Gln
                1                5                10

atg tcg acg aca tgc gat tcg ctt cta ctg gag ctc aat gtg att tgg      278
Met Ser Thr Thr Cys Asp Ser Leu Leu Leu Glu Leu Asn Val Ile Trp
                15                20                25

gat gag gtc ggt gag ccc gac acg acg agg gac agg atg ctg ctg gag      326
Asp Glu Val Gly Glu Pro Asp Thr Thr Arg Asp Arg Met Leu Leu Glu
                30                35                40

ctc gag cag gag tgc ctg gag gtc tac agg cgg aag gtc gac cag gcg      374
Leu Glu Gln Glu Cys Leu Glu Val Tyr Arg Arg Lys Val Asp Gln Ala
                45                50                55

aac cgg agc cgc gcc cag ctg cgg aag gcc atc gcc gag ggc gag gca      422
Asn Arg Ser Arg Ala Gln Leu Arg Lys Ala Ile Ala Glu Gly Glu Ala
                60                65                70                75

gag ctc gcc ggc atc tgc tca gcc atg ggc gag ccg ccc gtg cac gtt      470
Glu Leu Ala Gly Ile Cys Ser Ala Met Gly Glu Pro Pro Val His Val
                80                85                90

aga cag tca aat cag aag ctt cat ggc tta aga gag gag ttg aat gca      518
```

YAM20052.TXT

Arg	Gln	Ser	Asn 95	Gln	Lys	Leu	His	Gly 100	Leu	Arg	Glu	Glu	Leu	Asn	Ala		
att	gtt	ccg	tat	ttg	gaa	gaa	atg	aaa	aag	aaa	aag	gtc	gaa	cga	tgg	566	
Ile	Val	Pro 110	Tyr	Leu	Glu	Glu	Met 115	Lys	Lys	Lys	Lys	Val 120	Glu	Arg	Trp		
aac	cag	ttt	gtt	cat	gtc	ata	gag	cag	att	aag	aaa	att	tcg	tct	gaa	614	
Asn	Gln	Phe	Val	His	Val	Ile 130	Glu	Gln	Ile	Lys	Lys 135	Ile	Ser	Ser	Glu		
ata	agg	cca	gcc	gat	ttt	gtt	ccc	ttt	aaa	gtt	ccg	gtt	gat	cag	tct	662	
Ile	Arg	Pro	Ala	Asp	Phe 145	Val	Pro	Phe	Lys	Val 150	Pro	Val	Asp	Gln	Ser 155		
gac	ctg	tca	tta	aga	aag	ctt	gat	gag	ttg	acg	aag	gac	ctg	gaa	tcc	710	
Asp	Leu	Ser	Leu	Arg 160	Lys	Leu	Asp	Glu	Leu 165	Thr	Lys	Asp	Leu	Glu	Ser 170		
ctt	cag	aag	gag	aag	agc	gat	cgg	cta	aag	caa	gtg	ata	gaa	cat	ttg	758	
Leu	Gln	Lys	Glu 175	Lys	Ser	Asp	Arg	Leu 180	Lys	Gln	Val	Ile 185	Glu	His	Leu		
aat	tct	ttg	cat	tcc	tta	tgt	gag	gtg	ctt	ggc	ata	gat	ttc	aag	caa	806	
Asn	Ser	Leu 190	His	Ser	Leu	Cys	Glu 195	Val	Leu	Gly	Ile	Asp 200	Phe	Lys	Gln		
aca	gta	tat	gag	gtg	cac	cct	agc	ttg	gac	gaa	gct	gaa	gga	tca	aag	854	
Thr	Val 205	Tyr	Glu	Val	His	Pro 210	Ser	Leu	Asp	Glu	Ala 215	Glu	Gly	Ser	Lys		
aac	ctg	agc	aac	act	aca	att	gag	agg	ctt	gct	gct	gcc	gca	aac	aga	902	
Asn	Leu	Ser	Asn	Thr 225	Thr	Ile	Glu	Arg	Leu 230	Ala	Ala	Ala	Ala	Asn	Arg 235		
ctg	cgt	gaa	atg	aag	atc	caa	agg	atg	caa	aag	ctt	caa	gat	ttt	gct	950	
Leu	Arg	Glu	Met	Lys 240	Ile	Gln	Arg	Met	Gln 245	Lys	Leu	Gln	Asp	Phe 250	Ala		
tct	agc	atg	ctc	gag	cta	tgg	aat	ctc	atg	gat	act	cca	ctt	gaa	gag	998	
Ser	Ser	Met	Leu 255	Glu	Leu	Trp	Asn	Leu 260	Met	Asp	Thr	Pro	Leu 265	Glu	Glu		
cag	cag	atg	ttt	cag	aat	ata	aca	tgc	aat	att	gct	gct	tca	gaa	caa	1046	
Gln	Gln	Met 270	Phe	Gln	Asn	Ile	Thr 275	Cys	Asn	Ile	Ala	Ala 280	Ser	Glu	Gln		
gag	ata	act	gaa	cca	aac	acc	ctc	tcc	aca	gat	ttc	ctg	aat	tat	gtc	1094	
Glu	Ile 285	Thr	Glu	Pro	Asn	Thr 290	Leu	Ser	Thr	Asp	Phe 295	Leu	Asn	Tyr	Val		
gaa	tct	gag	gtg	tta	agg	ctt	gaa	caa	ctg	aaa	gca	agt	aag	atg	aaa	1142	
Glu	Ser	Glu	Val	Leu	Arg 305	Leu	Glu	Gln	Leu 310	Lys	Ala	Ser	Lys	Met	Lys 315		
gat	ctt	gtt	tta	aaa	aag	aaa	gca	gaa	cta	gaa	gag	cat	aga	aga	cgt	1190	
Asp	Leu	Val	Leu	Lys 320	Lys	Lys	Ala	Glu	Leu 325	Glu	Glu	His	Arg	Arg 330	Arg		
gct	cat	ctt	gtt	ggc	gag	gaa	ggg	tat	gca	gag	gag	ttt	agc	att	gaa	1238	
Ala	His	Leu	Val	Gly	Glu	Glu	Gly	Tyr	Ala	Glu	Glu	Phe	Ser	Ile	Glu		

YAM20052.TXT

335										340										345										
gct	att	gaa	gct	gga	gct	att	gat	ccc	tca	cta	gta	ctt	gaa	caa	att	1286														
Ala	Ile	Glu	Ala	Gly	Ala	Ile	Asp	Pro	Ser	Leu	Val	Leu	Glu	Gln	Ile															
		350					355					360																		
gaa	gct	cac	att	gca	aca	gtg	aaa	gag	gaa	gct	ttt	agc	cgg	aag	gat	1334														
Glu	Ala	His	Ile	Ala	Thr	Val	Lys	Glu	Glu	Ala	Phe	Ser	Arg	Lys	Asp															
	365					370					375																			
att	ctt	gag	aaa	gtt	gaa	aga	tgg	caa	aat	gct	tgt	gaa	gag	gaa	gcc	1382														
Ile	Leu	Glu	Lys	Val	Glu	Arg	Trp	Gln	Asn	Ala	Cys	Glu	Glu	Glu	Ala															
380					385					390					395															
tgg	ctg	gaa	gat	tac	aac	aaa	gat	gat	aat	cgt	tac	aat	gct	ggg	agg	1430														
Trp	Leu	Glu	Asp	Tyr	Asn	Lys	Asp	Asp	Asn	Arg	Tyr	Asn	Ala	Gly	Arg															
				400					405					410																
gga	gca	cat	cta	aca	cta	aag	agg	gct	gaa	aag	gct	cgt	act	ttg	gtc	1478														
Gly	Ala	His	Leu	Thr	Leu	Lys	Arg	Ala	Glu	Lys	Ala	Arg	Thr	Leu	Val															
			415					420					425																	
aac	aag	att	cct	gga	atg	gta	gat	gtt	ttg	aga	aca	aaa	att	gct	gca	1526														
Asn	Lys	Ile	Pro	Gly	Met	Val	Asp	Val	Leu	Arg	Thr	Lys	Ile	Ala	Ala															
		430					435					440																		
tgg	aaa	aat	gaa	cga	gga	aag	gag	gat	ttc	aca	tat	gat	ggt	gtt	agc	1574														
Trp	Lys	Asn	Glu	Arg	Gly	Lys	Glu	Asp	Phe	Thr	Tyr	Asp	Gly	Val	Ser															
	445					450					455																			
ctt	tcg	tca	atg	ctt	gat	gaa	tat	atg	ttc	gtt	cgt	cag	gag	aaa	gag	1622														
Leu	Ser	Ser	Met	Leu	Asp	Glu	Tyr	Met	Phe	Val	Arg	Gln	Glu	Lys	Glu															
460					465					470					475															
caa	gag	aag	aag	aga	caa	agg	gat	cag	aag	aag	ctc	cag	gat	cag	ctc	1670														
Gln	Glu	Lys	Lys	Arg	Gln	Arg	Asp	Gln	Lys	Lys	Leu	Gln	Asp	Gln	Leu															
				480					485					490																
aaa	gcg	gag	cag	gaa	gct	ttg	tac	gga	tca	aaa	ccc	agt	cca	tcc	aag	1718														
Lys	Ala	Glu	Gln	Glu	Ala	Leu	Tyr	Gly	Ser	Lys	Pro	Ser	Pro	Ser	Lys															
			495					500					505																	
ccc	cta	agt	aca	aag	aag	gca	cct	agg	cac	tct	atg	ggt	ggt	gca	aac	1766														
Pro	Leu	Ser	Thr	Lys	Lys	Ala	Pro	Arg	His	Ser	Met	Gly	Gly	Ala	Asn															
		510					515					520																		
cga	agg	cta	tct	ctt	ggt	gga	gcc	acc	atg	caa	ccc	ccg	aag	act	gat	1814														
Arg	Arg	Leu	Ser	Leu	Gly	Gly	Ala	Thr	Met	Gln	Pro	Pro	Lys	Thr	Asp															
	525					530					535																			
ata	ctg	cat	tca	aag	tct	gtt	cgt	gct	gcc	aag	aaa	act	gaa	gaa	atc	1862														
Ile	Leu	His	Ser	Lys	Ser	Val	Arg	Ala	Ala	Lys	Lys	Thr	Glu	Glu	Ile															
540					545					550					555															
ggc	act	ttg	tcc	cct	agt	agt	agt	aga	ggt	ttg	gac	att	gcc	gga	ttg	1910														
Gly	Thr	Leu	Ser	Pro	Ser	Ser	Ser	Arg	Gly	Leu	Asp	Ile	Ala	Gly	Leu															
				560					565					570																
cct	atc	aag	aag	ttg	tct	ttc	aat	gcc	agt	act	cta	cgt	gag	acg	gag	1958														
Pro	Ile	Lys	Lys	Leu	Ser	Phe	Asn	Ala	Ser	Thr	Leu	Arg	Glu	Thr	Glu															
			575					580					585																	

YAM20052.TXT

aca cct cgt aaa cct ttt gct cag atc aca cca gga aac agt gtc tcg 2006
 Thr Pro Arg Lys Pro Phe Ala Gln Ile Thr Pro Gly Asn Ser Val Ser
 590 595 600
 tcg acg cct gtg cgc cct atc acc aat aac act gag gat gat gag aac 2054
 Ser Thr Pro Val Arg Pro Ile Thr Asn Asn Thr Glu Asp Asp Glu Asn
 605 610 615
 agg act ccg aag aca ttt aca gca ctg aat ccc aag act ccg atg act 2102
 Arg Thr Pro Lys Thr Phe Thr Ala Leu Asn Pro Lys Thr Pro Met Thr
 620 625 630 635
 gtt acg gct cca atg cag atg gca atg act ccc tct ctg gcc aac aag 2150
 Val Thr Ala Pro Met Gln Met Ala Met Thr Pro Ser Leu Ala Asn Lys
 640 645 650
 gtt tca gca act cca gtt tcc ctt gtt tac gac aag cca gag gta aca 2198
 Val Ser Ala Thr Pro Val Ser Leu Val Tyr Asp Lys Pro Glu Val Thr
 655 660 665
 ttg cag gag gac atc gac tac tcc ttt gaa gaa agg cgg ctc gcc atc 2246
 Leu Gln Glu Asp Ile Asp Tyr Ser Phe Glu Glu Arg Arg Leu Ala Ile
 670 675 680
 tat ctg gcc agg caa atg gtt taa ctgttgatca atttatgtac gtagttgaaa 2300
 Tyr Leu Ala Arg Gln Met Val
 685 690
 tctgactgca ttttcttgtc ggtggccatt gcgtatgttg gtcaacaata gtcggccttt 2360
 ccagtagcac tattctgatt tactgcaatt gttttaatgt tttctacaac cagtaaaaca 2420
 gctctataca ttagcttgct cactaaaaaa aaaaaaaaaa aaaaaaaaaa 2468

<210> 2

<211> 690

<212> PRT

<213> Oryza sativa

<400> 2

Met Ser Ser Ala Val Lys Asp Gln Leu His Gln Met Ser Thr Thr Cys
 1 5 10 15
 Asp Ser Leu Leu Leu Glu Leu Asn Val Ile Trp Asp Glu Val Gly Glu
 20 25 30
 Pro Asp Thr Thr Arg Asp Arg Met Leu Leu Glu Leu Glu Gln Glu Cys
 35 40 45
 Leu Glu Val Tyr Arg Arg Lys Val Asp Gln Ala Asn Arg Ser Arg Ala
 50 55 60
 Gln Leu Arg Lys Ala Ile Ala Glu Gly Glu Ala Glu Leu Ala Gly Ile
 65 70 75 80
 Cys Ser Ala Met Gly Glu Pro Pro Val His Val Arg Gln Ser Asn Gln
 85 90 95
 Lys Leu His Gly Leu Arg Glu Glu Leu Asn Ala Ile Val Pro Tyr Leu
 100 105 110
 Glu Glu Met Lys Lys Lys Lys Val Glu Arg Trp Asn Gln Phe Val His
 115 120 125
 Val Ile Glu Gln Ile Lys Lys Ile Ser Ser Glu Ile Arg Pro Ala Asp
 130 135 140
 Phe Val Pro Phe Lys Val Pro Val Asp Gln Ser Asp Leu Ser Leu Arg
 145 150 155 160
 Lys Leu Asp Glu Leu Thr Lys Asp Leu Glu Ser Leu Gln Lys Glu Lys
 165 170 175

YAM20052.TXT

Ser Asp Arg Leu Lys Gln Val Ile Glu His Leu Asn Ser Leu His Ser
 180 185 190
 Leu Cys Glu Val Leu Gly Ile Asp Phe Lys Gln Thr Val Tyr Glu Val
 195 200 205
 His Pro Ser Leu Asp Glu Ala Ala Ala Asn Arg Leu Ser Asn Thr
 210 215 220
 Thr Ile Glu Arg Leu Ala Ala Ala Asn Arg Leu Arg Glu Met Lys
 225 230 235 240
 Ile Gln Arg Met Gln Lys Leu Gln Asp Phe Ala Ser Ser Met Leu Glu
 245 250 255
 Leu Trp Asn Leu Met Asp Thr Pro Leu Glu Glu Gln Gln Met Phe Gln
 260 265 270
 Asn Ile Thr Cys Asn Ile Ala Ala Ser Glu Gln Glu Ile Thr Glu Pro
 275 280 285
 Asn Thr Leu Ser Thr Asp Phe Leu Asn Tyr Val Glu Ser Glu Val Leu
 290 295 300
 Arg Leu Glu Gln Leu Lys Ala Ser Lys Met Lys Asp Leu Val Leu Lys
 305 310 315 320
 Lys Lys Ala Glu Leu Glu Glu His Arg Arg Arg Ala His Leu Val Gly
 325 330 335
 Glu Glu Gly Tyr Ala Glu Glu Phe Ser Ile Glu Ala Ile Glu Ala Gly
 340 345 350
 Ala Ile Asp Pro Ser Leu Val Leu Glu Gln Ile Glu Ala His Ile Ala
 355 360 365
 Thr Val Lys Glu Glu Ala Phe Ser Arg Lys Asp Ile Leu Glu Lys Val
 370 375 380
 Glu Arg Trp Gln Asn Ala Cys Glu Glu Glu Ala Trp Leu Glu Asp Tyr
 385 390 395 400
 Asn Lys Asp Asp Asn Arg Tyr Asn Ala Gly Arg Gly Ala His Leu Thr
 405 410 415
 Leu Lys Arg Ala Glu Lys Ala Arg Thr Leu Val Asn Lys Ile Pro Gly
 420 425 430
 Met Val Asp Val Leu Arg Thr Lys Ile Ala Ala Trp Lys Asn Glu Arg
 435 440 445
 Gly Lys Glu Asp Phe Thr Tyr Asp Gly Val Ser Leu Ser Ser Met Leu
 450 455 460
 Asp Glu Tyr Met Phe Val Arg Gln Glu Lys Glu Gln Glu Lys Lys Arg
 465 470 475 480
 Gln Arg Asp Gln Lys Lys Leu Gln Asp Gln Leu Lys Ala Glu Gln Glu
 485 490 495
 Ala Leu Tyr Gly Ser Lys Pro Ser Pro Ser Lys Pro Leu Ser Thr Lys
 500 505 510
 Lys Ala Pro Arg His Ser Met Gly Gly Ala Asn Arg Arg Leu Ser Leu
 515 520 525
 Gly Gly Ala Thr Met Gln Pro Lys Thr Asp Ile Leu His Ser Lys
 530 535 540
 Ser Val Arg Ala Ala Lys Lys Thr Glu Glu Ile Gly Thr Leu Ser Pro
 545 550 555 560
 Ser Ser Ser Arg Gly Leu Asp Ile Ala Gly Leu Pro Ile Lys Lys Leu
 565 570 575
 Ser Phe Asn Ala Ser Thr Leu Arg Glu Thr Glu Thr Pro Arg Lys Pro
 580 585 590
 Phe Ala Gln Ile Thr Pro Gly Asn Ser Val Ser Ser Thr Pro Val Arg
 595 600 605
 Pro Ile Thr Asn Asn Thr Glu Asp Asp Glu Asn Arg Thr Pro Lys Thr
 610 615 620
 Phe Thr Ala Leu Asn Pro Lys Thr Pro Met Thr Val Thr Ala Pro Met
 625 630 635 640
 Gln Met Ala Met Thr Pro Ser Leu Ala Asn Lys Val Ser Ala Thr Pro
 645 650 655
 Val Ser Leu Val Tyr Asp Lys Pro Glu Val Thr Leu Gln Glu Asp Ile
 660 665 670
 Asp Tyr Ser Phe Glu Glu Arg Arg Leu Ala Ile Tyr Leu Ala Arg Gln

Met Val
690

675

680

685

<210> 3
<211> 4574
<212> DNA
<213> Oryza sativa

<400> 3

aaaaaaatat	ttcaaatcac	actacactct	ccgtcgtctc	ctctcctctc	ctctcctccc	60
cctctcctcc	gcctctctcg	catctgaggc	tccgatcgcc	ggcgacccca	gccagaatcc	120
gccgccccgt	ctcgccctcc	ccgctcgacg	agaccgcgcc	gagcggcgaa	gaggcctagt	180
gttcttcgca	cctcgcgatg	agtagcgcg	tgaaggacca	gcttcaccag	atgtcgacga	240
catgcgattc	gcttctactg	gagctcaatg	tatgtcaccg	cttgccgatt	caaccatttc	300
ccggctactc	gtgttggttc	tggcatggca	gtggaggatt	tacggggttt	ttttcttctc	360
tcgttctgtt	tcaggtgatt	tgggatgagg	tcggtgagcc	cgacacgacg	agggacagga	420
tgctgctgga	gctcgagcag	gagtgcctgg	aggctctacg	gcggaaggctc	gaccaggcga	480
accggagccg	cgcccagctg	cggaaggcca	tcgccgaggg	cgaggcagag	ctcgccggca	540
tctgctcagc	catgggcgag	ccgcccgtgc	acgttagaca	ggttagtttc	tggctccacc	600
aatggctgta	aaagagggtat	cgcatggttg	gatcaaaaga	tggaagtcga	attcctgttg	660
aactgtgcta	attggcgatg	gaagaaaagg	aagatttagt	agagaactaa	aagctacgat	720
ttctgttgta	agatgatagt	actactgctt	gcattgttga	tctgatggag	gtaaaccgtg	780
tagaactcca	tcagcagtta	acatttttct	aactgattag	tagtagcgta	tcaatatatt	840
aagggaaagt	gttggcagag	cttacatttc	tttctcactt	ctattctcga	ctttatgccc	900
agttactgct	caatcggttc	tatacttttt	actgctgttc	ccatgcatta	gcaatttagg	960
atatatgttt	tgtaaaaattt	atctgtttcc	ttcagtttga	atatgttcag	catgaataat	1020
atatttactg	ttttaccggc	agcatgacta	agttactgcc	tcaagtacgt	tttatttggt	1080
gaatacattc	taccttcttg	actaatcaat	tctgcttgac	tgtagatttt	agcacttcct	1140
cagccattca	tgcagtaaca	tgcatttcac	ctgaaatttt	gcagtcaaat	cagaagcttc	1200
atggcttaag	agaggagtgg	aatgcaattg	ttccgtattt	ggaagaaatg	aaaaagaaaa	1260
aggtcgaacg	atggaaccag	tttgttcatg	tcatagagca	gattaagaaa	atttcgtctg	1320
aaataaggcc	agccgatttt	gttcccttta	aagttccggg	tgatcagctc	gacctgtcat	1380
taagaaagct	tgtatgattg	acgaaggacc	ttgaatccct	tcagaaggag	aaggctcatc	1440
tcactaatac	catctttatc	cattttcacc	agtcattgtg	tcacgtgtgc	tctatctatc	1500
aagaatcctt	ttcatttctt	gtataaaatc	tcactatgcc	atatacatgt	ttgtttctca	1560
cagagcgatc	ggctaaagca	agtgatagaa	catttgattt	ctttgcattc	cttatgtgag	1620
gtgcttgga	tagatttcaa	gcaaacagta	tatgaggtgc	accctagctt	ggacgaagct	1680
gaagagctaa	agaacctgaa	caacactaca	attgagaggc	ttgctgctgc	cgcaaacaga	1740
ctgcgtgaaa	tgaagatcca	aaggatcgaa	aaggtcagca	ttgcctgtac	cattgtagag	1800
gtatcaatga	acactttcag	tccttaactt	ggttaatctg	attctggcag	cttcaagatt	1860
ttgcttctag	catgctcgag	ctatggaatc	tcattggatac	tccacttgaa	gagcagcaga	1920
tgtttcagaa	tataacatgc	aattattgctg	cttcagaaca	agagataact	gaaccaaaca	1980
ccctctccac	agatttcctg	aattatgtaa	tttatcatca	ctgagattgc	aaaaatttat	2040
gttcgtactg	tgttatattt	tcattaagat	atgaatgttc	atcgactata	cttataactg	2100
taggtcgaat	ctgaggtggt	aaggcttgaa	caactgaaag	caagtaagat	gaaagatctt	2160
gttttaaaaa	agaaagcaga	actagaagag	catagaagac	gtgctcatct	tgttggcgag	2220
gaagggttatg	cagaggagt	tagcattgaa	gctattgaag	ctggttaagat	actctcctgc	2280
cttactgcct	tttattgtgc	ctgacaagtc	ataccagaca	gagttcatat	acctggtctg	2340
tgttctgttc	gcaggagcta	ttgatccctc	actagtactt	gaacaaattg	aagctcacat	2400
tgcaacagtg	aaagaggaag	cttttagccg	gaaggatatt	cttgagaaaag	ttgaaagatg	2460
gcaaaatgct	tgtgaaggag	aagcctggct	ggaagattac	aacaaagtat	ggatgctagc	2520
tgaagctacg	tggtctttgt	atatttggtt	agcaaataat	gtggtactga	tatctcctgg	2580
ctttggcttt	ttttaggatg	ataatcgtta	caatgctggg	aggggagcac	atctaact	2640
aaagagggct	gaaaaggctc	gtactttggt	caacaagatt	cctggtaatg	ttactcaatg	2700
atttatgtgt	ttggaacttc	cttatcaagt	gcatatttaa	tttacaattt	taactcttgc	2760
cttactacata	atctgatatt	ctgctgattg	gtctgagca	ggaatggtag	atgttttgag	2820
aacaaaaatt	gctgcatgga	aaaatgaacg	aggaaaggag	gatttcacat	atgatggtgt	2880
aggttttctt	actcttacac	attacattga	tcgggtctat	ttttgtttct	tgctgaagtg	2940
cctttcttgc	aattcttaca	ggtttagcct	tcgtcaatgc	ttgatgaata	tatgttcggt	3000
cgtcaggaga	aagagcaaga	gaagaagaga	caaagggtat	tatgctctcg	cctaataattc	3060
atgtattgtc	taaatcatct	tttcaccttc	tgtgaatacg	ctctaatact	tgaatataacc	3120

YAM20052.TXT

```

tgcaggatca gaagaagctc caggatcagc tcaaagcgga gcaggaagct ttgtacggat 3180
caaaacccag tccatccaag cccctaagta caaagaaggc acctaggcac tctatgggtg 3240
gtgcaaaccg aaggctatct cttggtggag ccaccatgca acccccgaag actgatatac 3300
tgcattcaaa gtctgttcgt gctgccaaaga aaactgaaga aatcggcact ttgtccccta 3360
gtaagcccta ctagctatca tgtgtcgata tatttctttt tcctcttatt ttcacttgaa 3420
catatgtcta actcaagcaa acaatatcag gtagtagagg tttggacatt gccggattgc 3480
ctatcaagaa gttgtctttc aatgccagta ctctacgtga gacggagaca cctcgtaaac 3540
cttttgctca gatcacacca ggaaacagtg tctcgtcgac gcctgtgcgc cctatcacca 3600
ataacactga ggatgatgag aacaggactc cgaagacatt tacagcactg aatcccaaga 3660
ctccgatgac tgttacggct ccaatgcaga tggcaatgac tccctctctg gccacaagg 3720
tttcagcaac tccagtttcc cttgtttacg acaagccaga ggtaacattg caggaggaca 3780
tcgactactc ctttgaagaa aggcggctcg ccatctatct ggccaggcaa atggtttaac 3840
tggtgatcaa tttatgtacg tagttgaaat ctgactgcat tttcttgctg gtggccattg 3900
cgtatgttgg tcaacaatag tcggcctttc cagtagcact attctgattt actgcaattg 3960
ttttaatgtt ttctacaacc agtaaaacag ctctatacat tagcttgctc actactcagt 4020
acagctttct cggcagcacg aaacatttct gttctctttg atgaatactt cttgctgtgg 4080
ataggatag ttactgttac atatactgta tgcccttcag aatagaaacc tgtagtacg 4140
ggaggtatta taggaaggat cgttttggaa ttttgggtgg tagcctgcac agtaagtcc 4200
atcagtttct ggattgtccc tcgcaaagaa aaaagtttct ttgattctgg taattcgttt 4260
gtcccacctg actccttgaa agtcttctgg acatgggaag ctatcgatc gtatcgctcg 4320
ggcgaacatg atgtgtgtgt cactctcgag tgagcaggcc accgaaggct gacttgactg 4380
actccagcaa ccaacaaacg agccagtcac ttttcacccc gggtttttgt cccaaaacac 4440
ttttccacca ccgtcaagcc tcaagcaaaa ccaaaacgct acgtaacgcc catcaacacc 4500
atgaaatcga gcagctagtt gtgcctgcta ctggccccc agtgccctgt accgcccgtt 4560
cttctcactc gaca                                     4574

```

<210> 4
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222>
 <223> PCR primer

<400> 4

gagagcatca tcggttacat cttctc

26

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> primer_bind
 <222>
 <223> PCR primer

<400> 5

atccaccttg agtttgaagg g

21

<210> 6
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 6

catcggatgt ccagtccatt g

21

<210> 7

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 7

acggagacac ctcgtaaacc

20

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 8

aaggccgact attgttgacc

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 9

cctgcaatgt tacctctggc

20

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 10

tgacaggtca gactgatcaa ccgg

24

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 11

taggcaatcc ggcaatgtcc

20

<210> 12

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 12

ctagaagcaa aatcttgaag ctgc

24

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 13

agtggtcttc gcacctcgcg

20

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 14

tgccctcgccc tcggcgatgg

20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<221> primer_bind

<222>

<223> PCR primer

<400> 15

aatatttcaa atcacactac

20